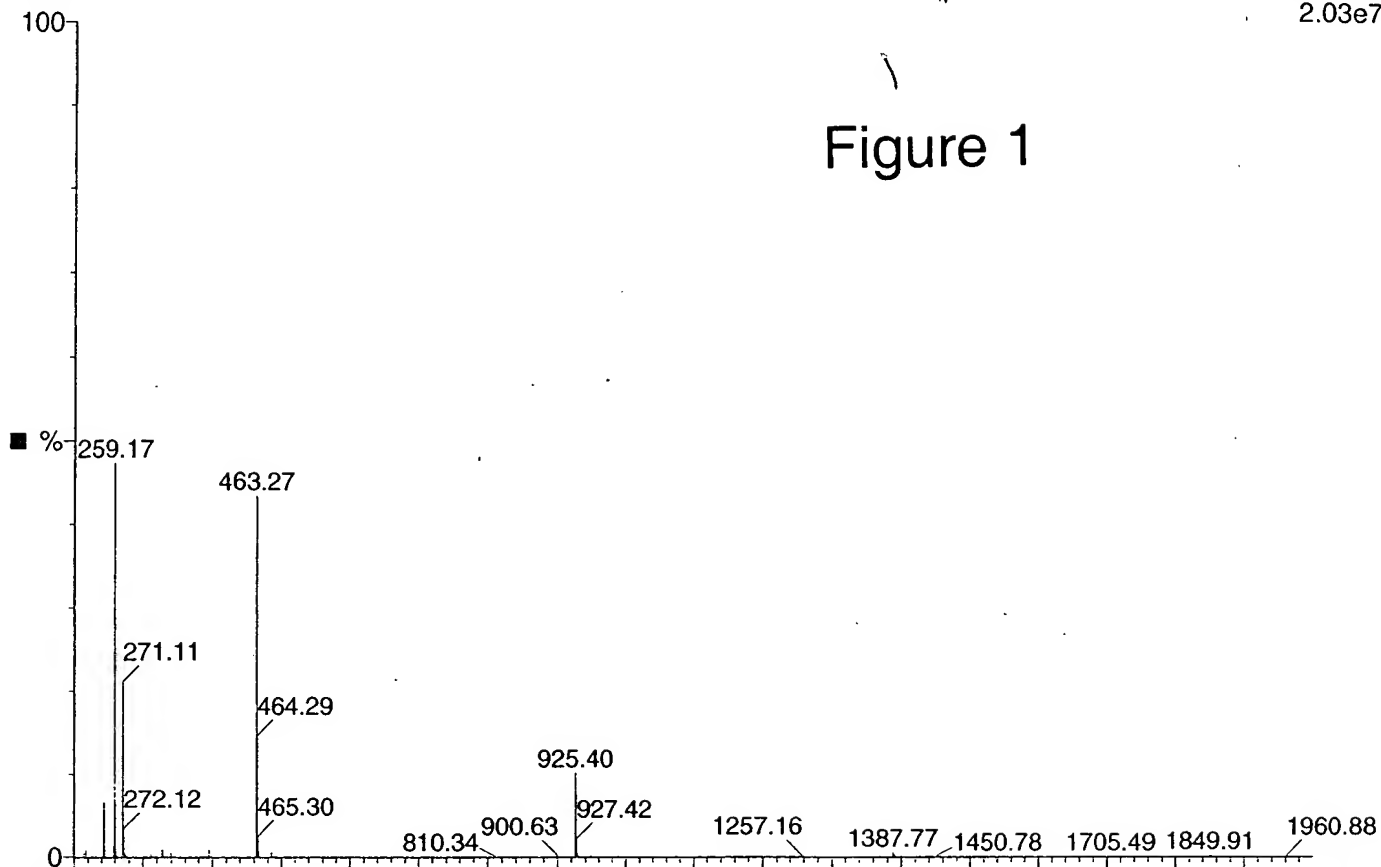


ECO04601Batch134_024_01_R1

ECO04601Batch134_024_01_R1 900 (45.030)

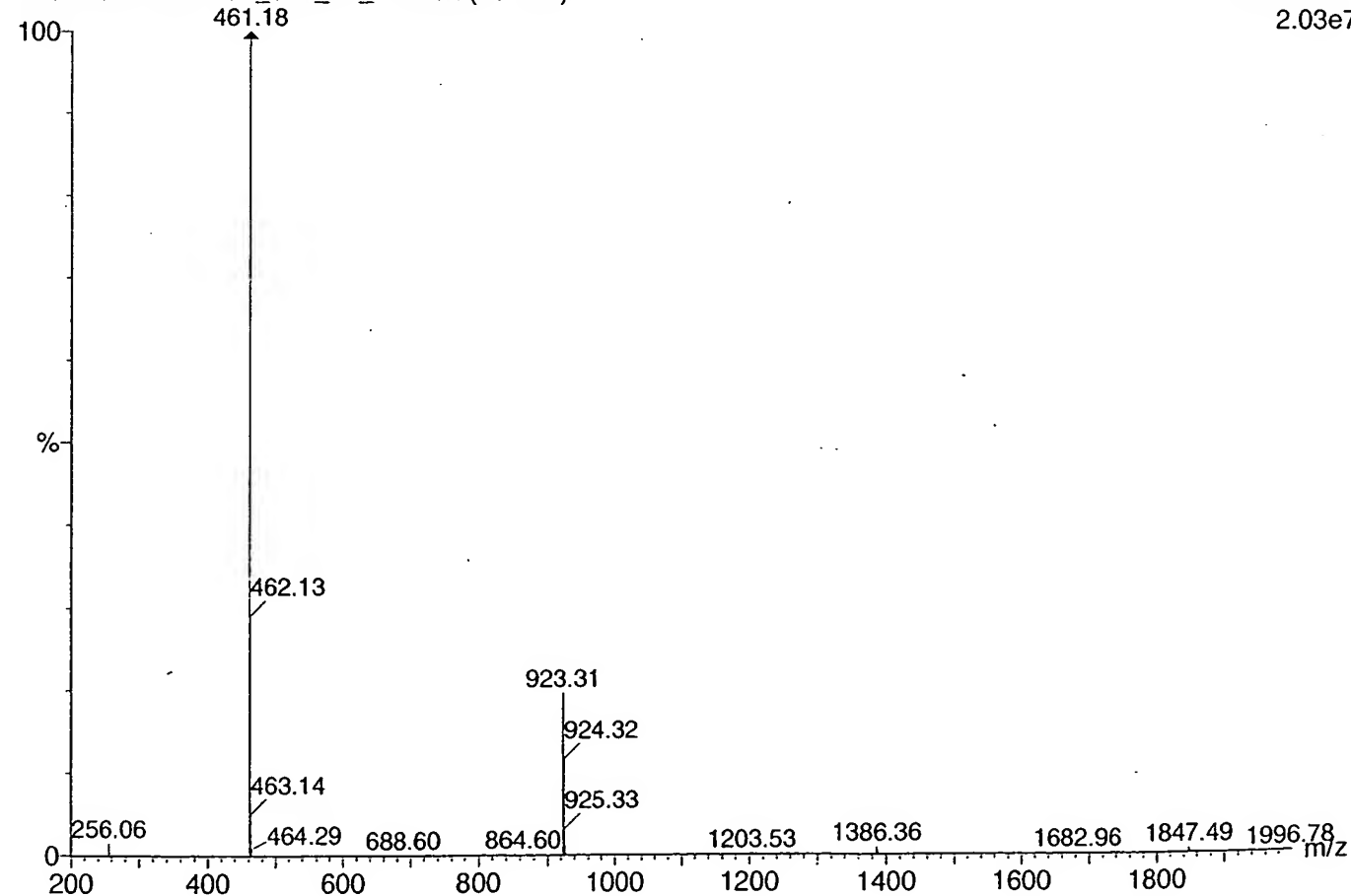
2: Scan ES+
2.03e7

Figure 1



ECO04601Batch134_024_01_R1 902 (45.105)

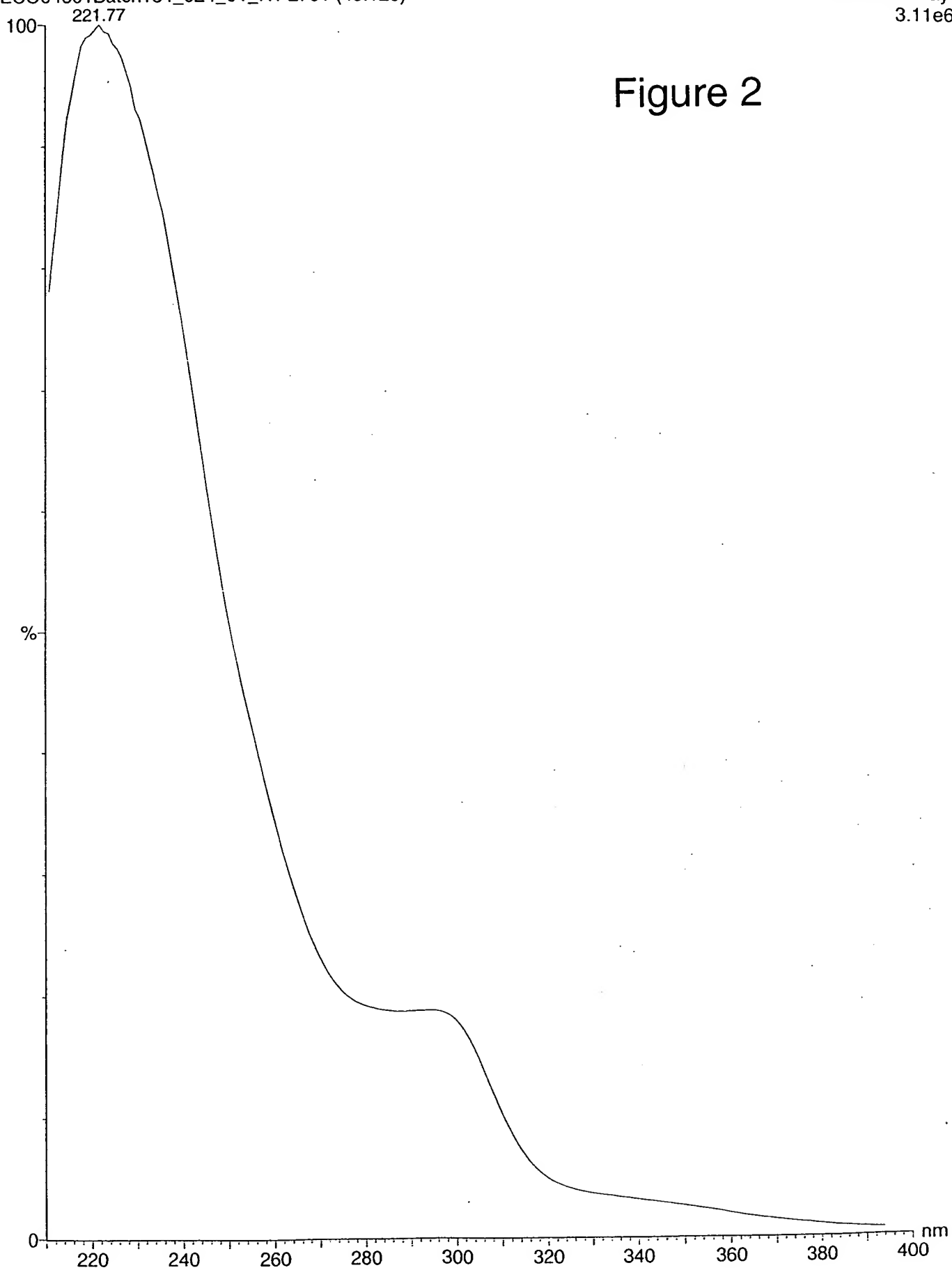
1: Scan ES-
2.03e7



ECO04601Batch134_024_01_R1
ECO04601Batch134_024_01_R1 2701 (45.120)

3: Diode Array
3.11e6

Figure 2



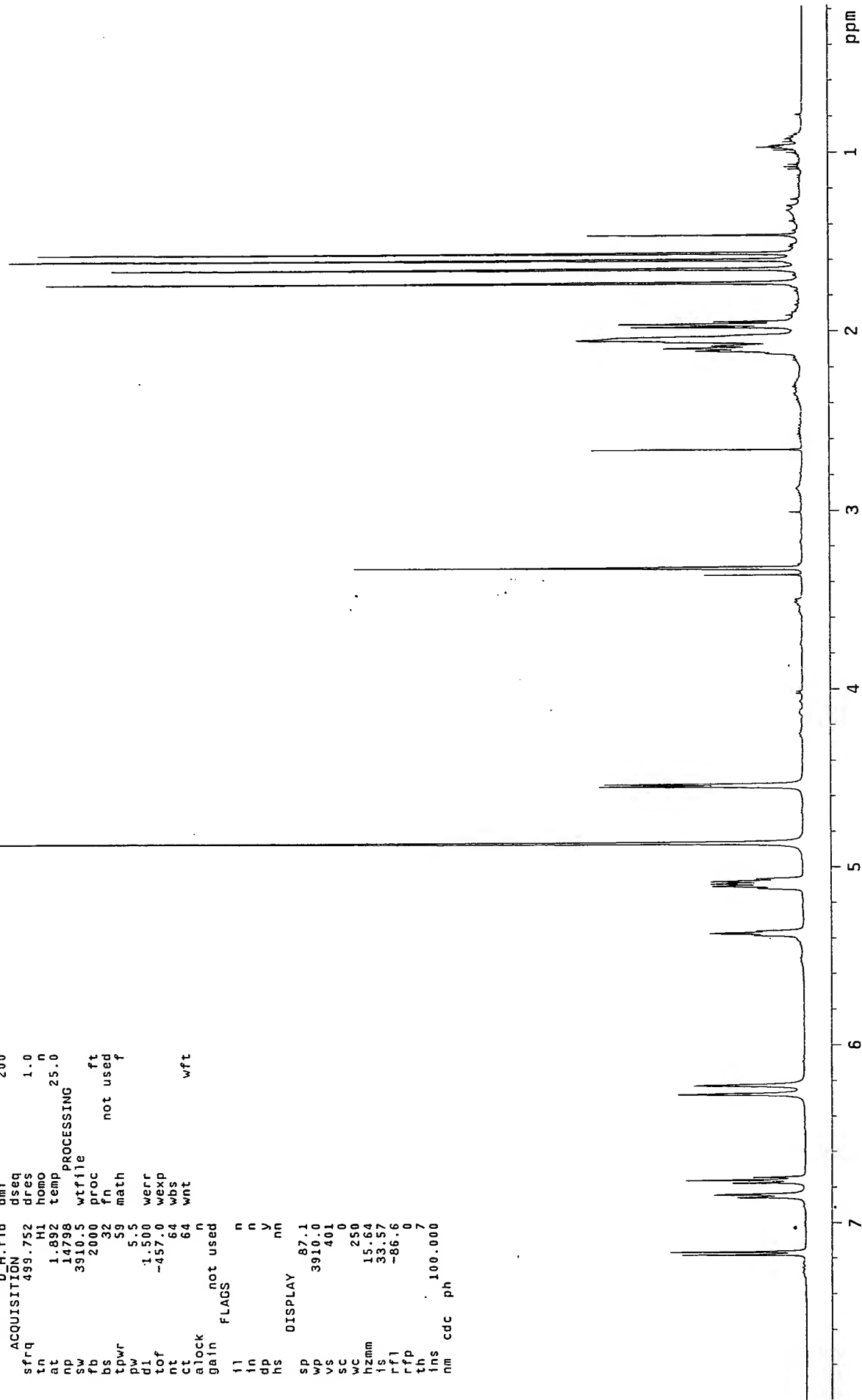
S01_046CIA07019e1002_run2_CD300_H

exp1 s2pu1

```

SAMPLE          DEC. & VT
date Jan 9 2004  dfrq 499.752
solvent CD300    dn   H1
file /import/thor/~ dpwr 30
ebiochem/NMR_Data/m~ dof 0
orris/S01_046CIA07~ dm  nnn
019e1002_run2_CD30~ dmm c
D_H.fid         dmf 200
ACQUISITION
sfrq 499.752    dres 1.0
tn      H1      homo n
at      1.892    temp 25.0
np      14798
sw      3910.5  wtfile
fb      2000    proc   ft
bs      32      fn     not used
tpwr    59      math   f
pw      5.5
dl      1.500   werr
tof     -457.0  wexp
nt      64      wbs
ct      64      wnt
a1ock   n
gain    not used
FLAGS
  ll      n
  ln      n
  dp      y
  hs      nn
  DISPLAY 87.1
  wp      3910.0
  vs      401
  sc      0
  wc      250
  hzmm    15.64
  ls      33.57
  rfl     -86.6
  rfp     0
  th      7
  ns      100.000
nm cdc ph
```

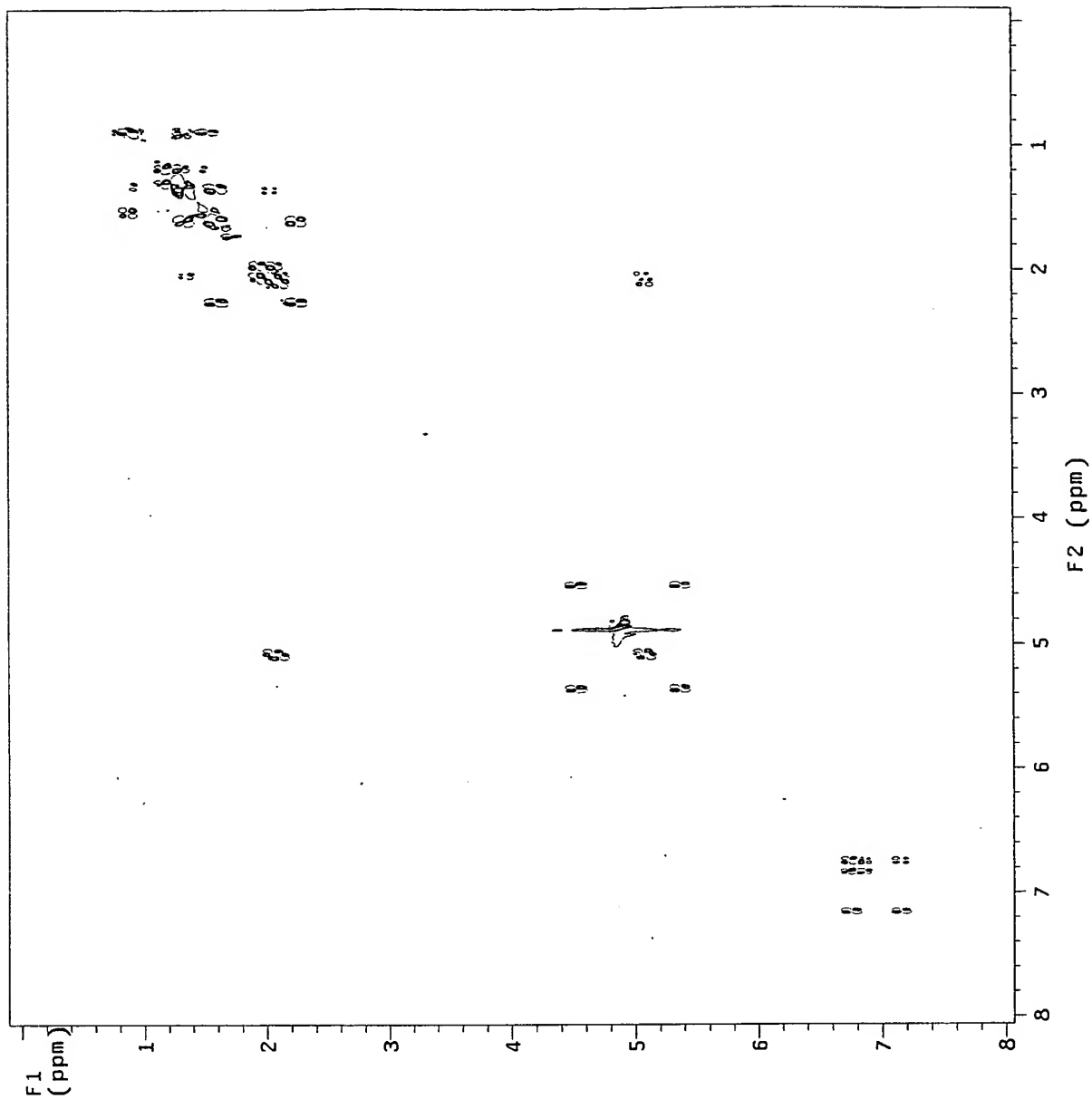
Figure 3



STANDARD PROTON PARAMETERS

Pulse Sequence: gDQCOSY
 Solvent: CD3OD
 Ambient temperature
 File: ECO04601_DQCOSY_CD3OD
 INOVA-500 "resonance"
 Relax. delay 1.000 sec
 Acq. time 0.125 sec
 Width 4085.0 Hz
 20 Width 4085.0 Hz
 16 repetitions
 2 x 102 increments
 OBSERVE H1, 499.7495793 MHz
 DATA PROCESSING
 Sq. sine bell 0.125 sec
 Shifted by -0.125 sec
 F1 DATA PROCESSING
 Sq. sine bell 0.025 sec
 Shifted by -0.025 sec
 FT size 2048 x 2048
 Total time 1 hr, 3 min, 46 sec

Figure 4



STANDARD PROTON PARAMETERS

Pulse Sequence: ghsqc

Solvent: CD300

Ambient temperature

File: EC004601_ghsQC_CD300

INOVA-500 "resonance"

Relax. delay 1.000 sec

Acq. time 0.125 sec

Width 4085.0 Hz

20 Width 22618.0 Hz

64 repetitions

2 x 128 increments

OBSERVE H1, 499.7495793 MHz

DECOUPLE C13, 125.6734093 MHz

Power 41 dB

on during acquisition

off during delay

W40 id4719 modulated

DATA-PROCESSING

Sq. sine bell 0.125 sec

Shifted by -0.125 sec

F1 DATA PROCESSING

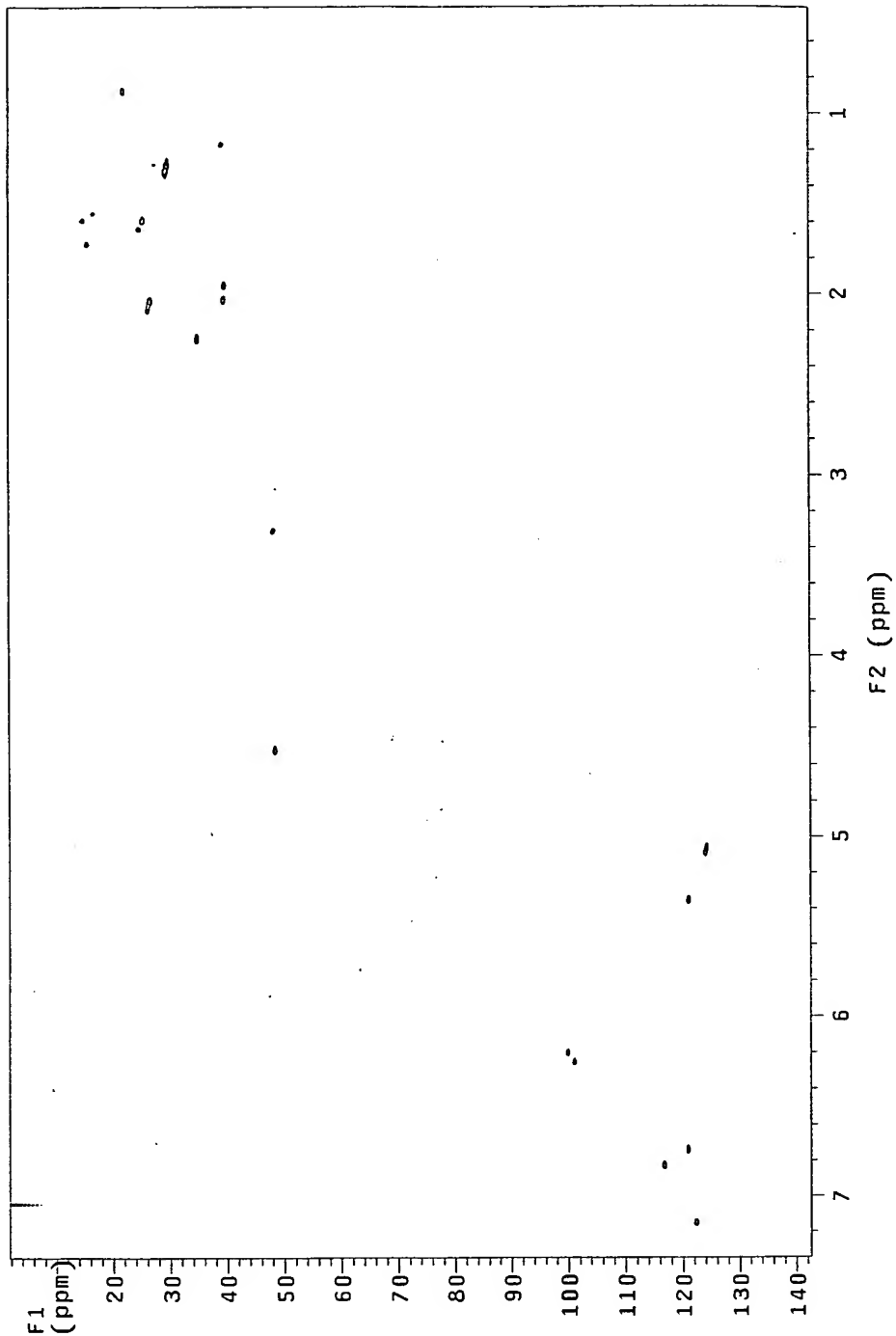
Sq. sine bell 0.023 sec

Shifted by -0.023 sec

FT size 2048 x 2048

Total time 5 hr, 27 min, 23 sec

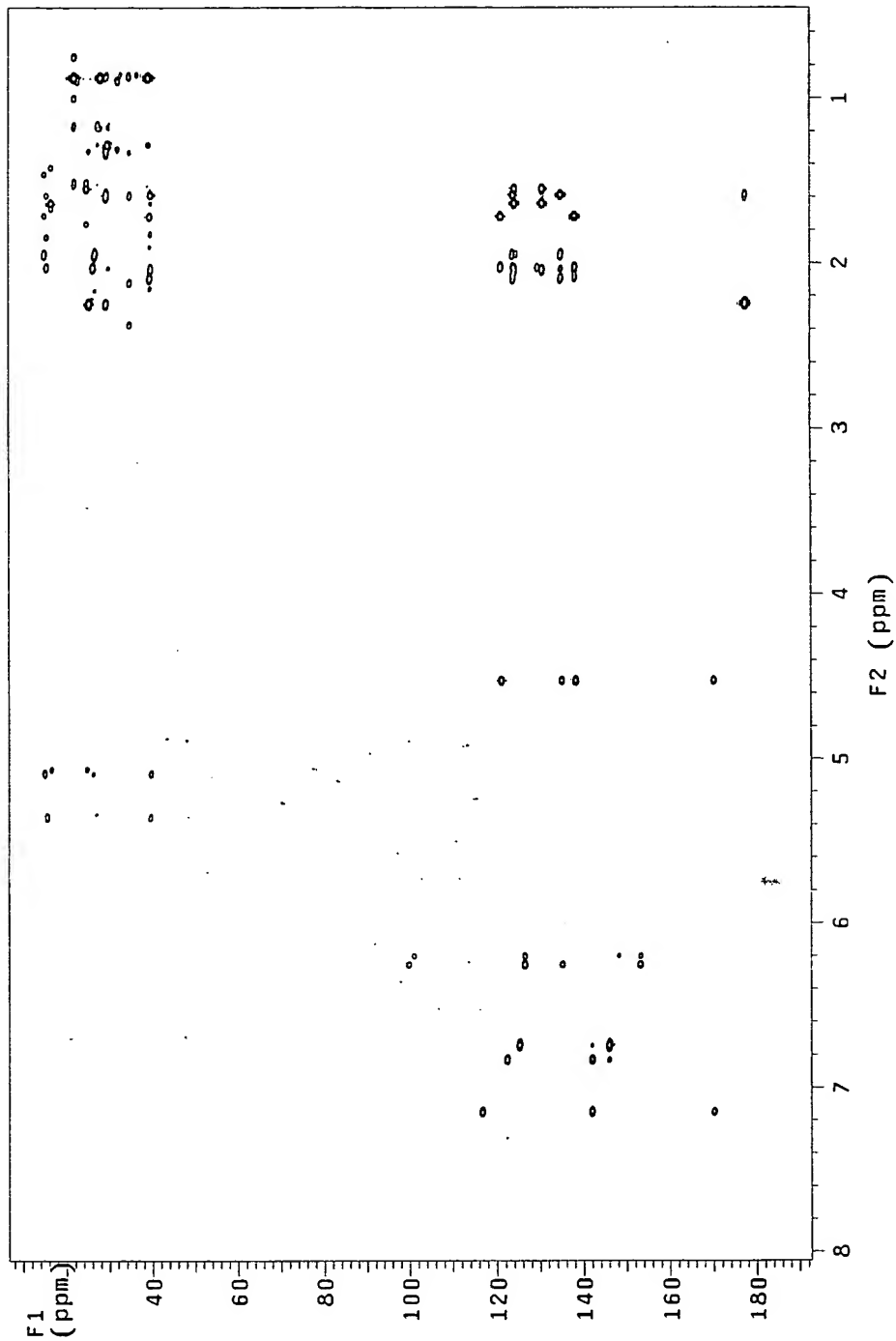
Figure 5



STANDARD PROTON PARAMETERS

Pulse Sequence: gHMBC
 Solvent: CD300
 Ambient temperature
 File: EC004601_HMBC2_CD300
 INOVA-500 "resonance"
 Relax. delay 1.000 sec
 Acq. time 0.125 sec
 Width 4085.0 Hz
 20 Width 28301.7 Hz
 64 repetitions
 400 increments
 OBSERVE H1, 499.7495793 MHz
 DATA PROCESSING
 Sine bell 0.063 sec
 F1 DATA PROCESSING
 Sine bell 0.007 sec
 FT size 2048 x 8192
 Total time 8 hr, 33 min, 13 sec

Figure 6



STANDARD PROTON PARAMETERS

Pulse Sequence: NOESY
 Solvent: CD300
 Ambient temperature
 File: noesy_brian_august09_2002
 INOVA-500 "resonance"
 Relax. delay 1.000 sec
 Mixing 0.600 sec
 Acq. time 0.125 sec
 Width 4085.0 Hz
 2D Width 4085.0 Hz
 16 repetitions
 2 x 256 increments
 OBSERVE H1, 499.7495793 MHz
 DATA PROCESSING
 Sg. sine bell 0.125 sec
 Shifted by -0.125 sec
 F1 DATA PROCESSING
 Sg. sine bell 0.063 sec
 Shifted by -0.063 sec
 FT size 4096 x 4096
 Total time 4 hr, 2 min, 2 sec

Figure 7

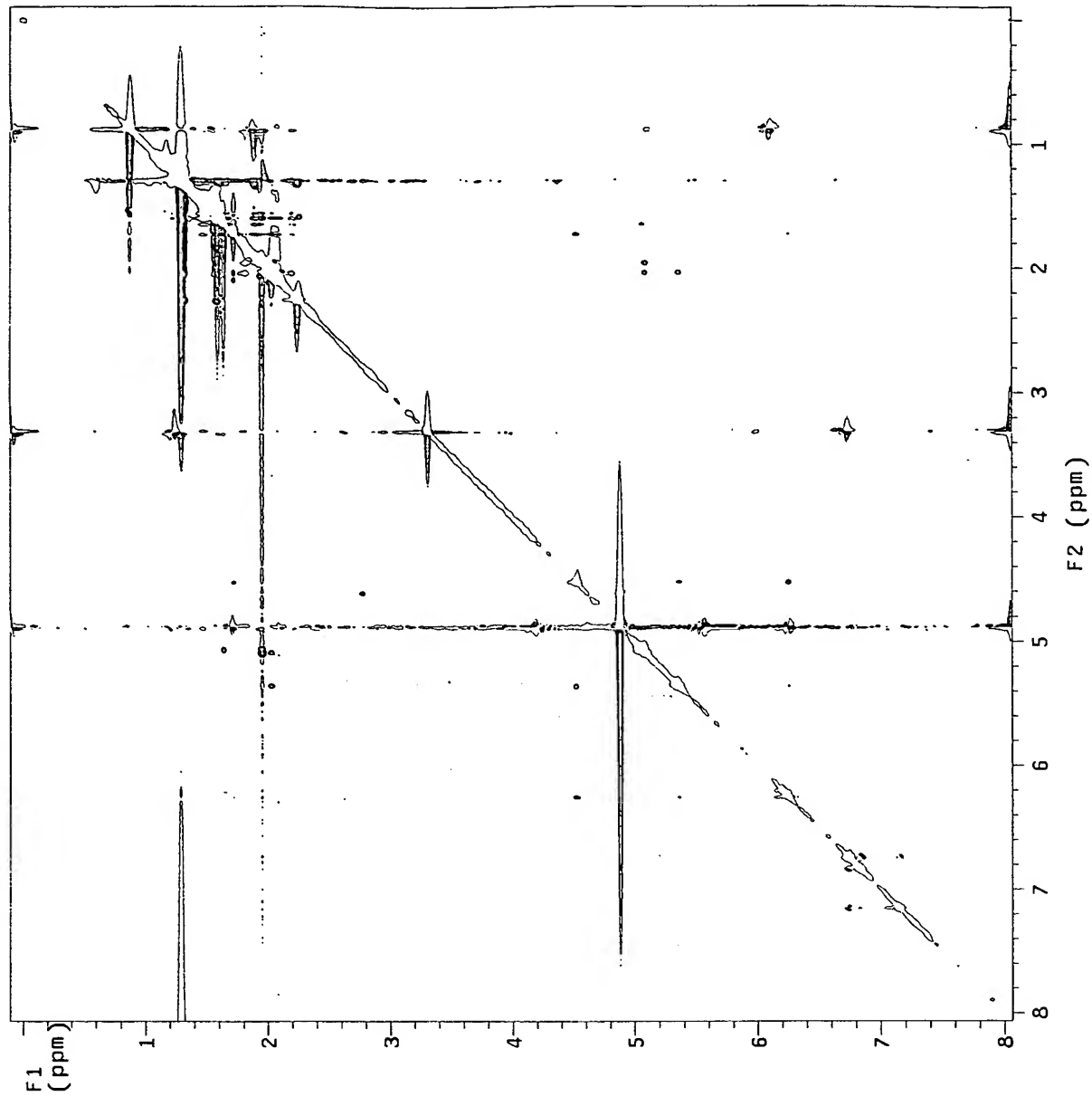


Figure 8

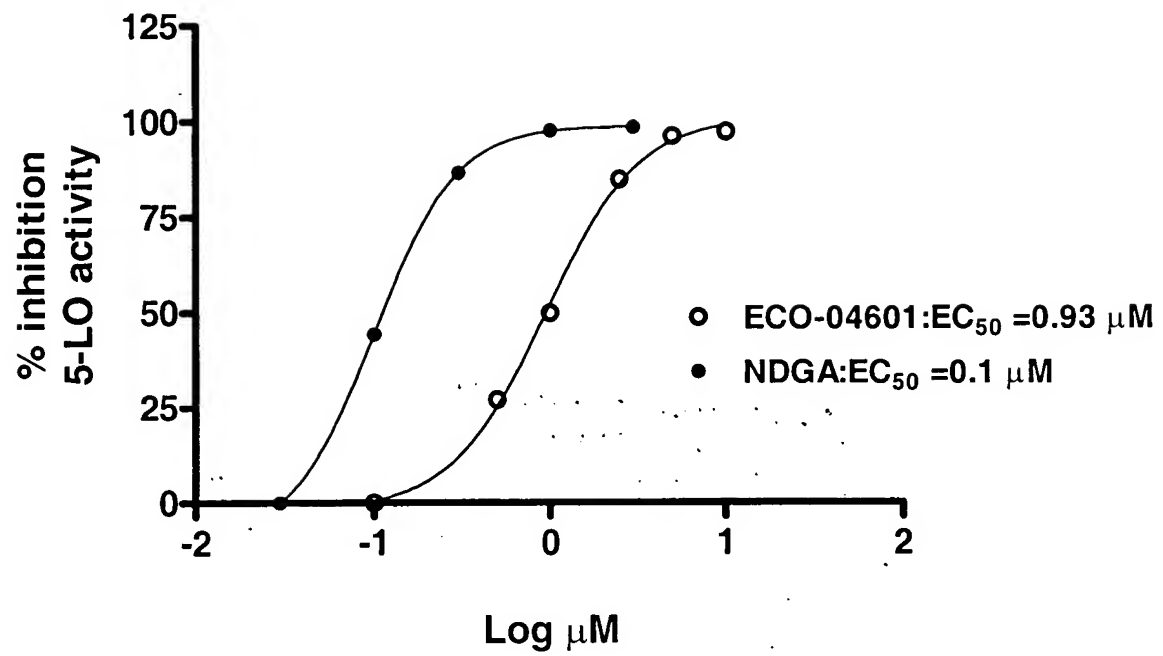


Figure 9

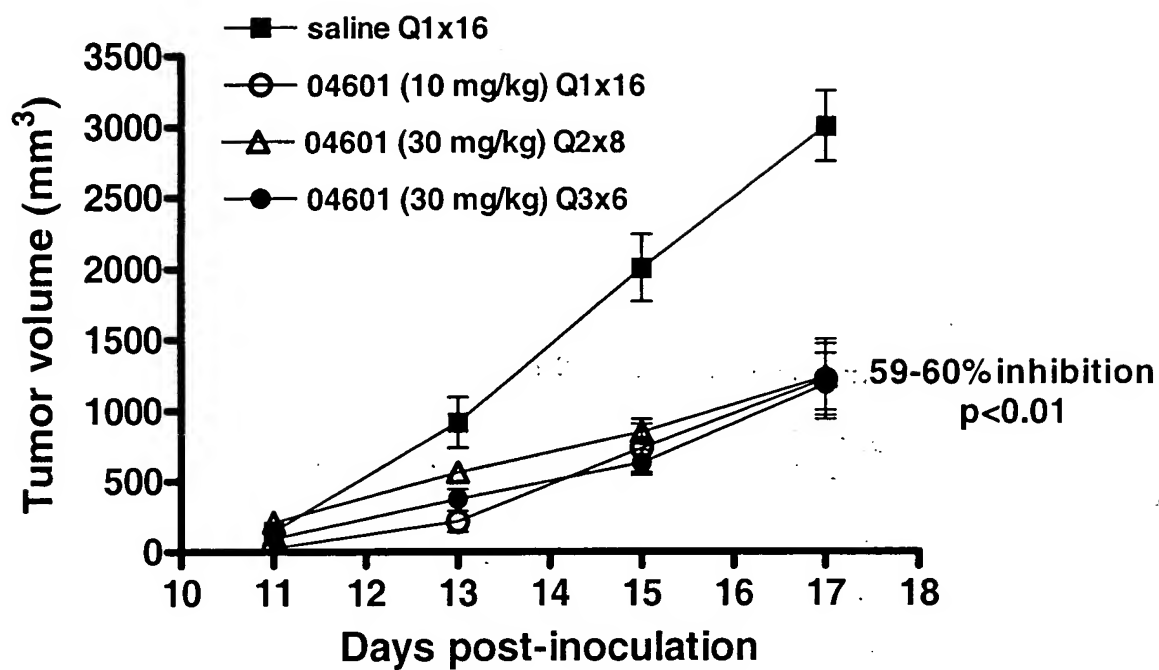


Figure 10

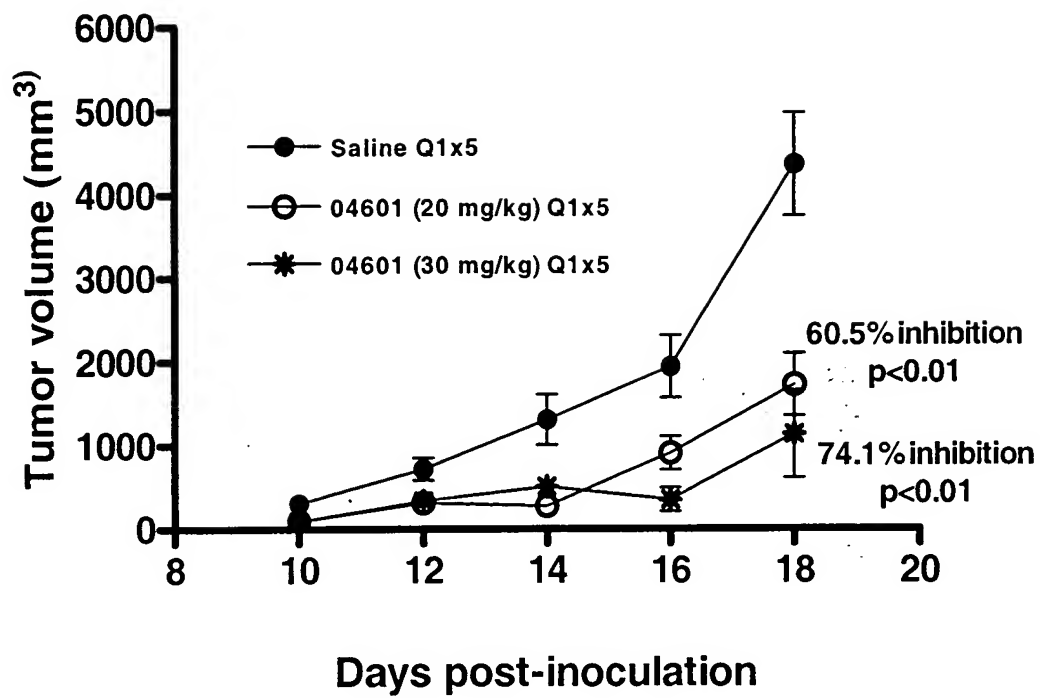
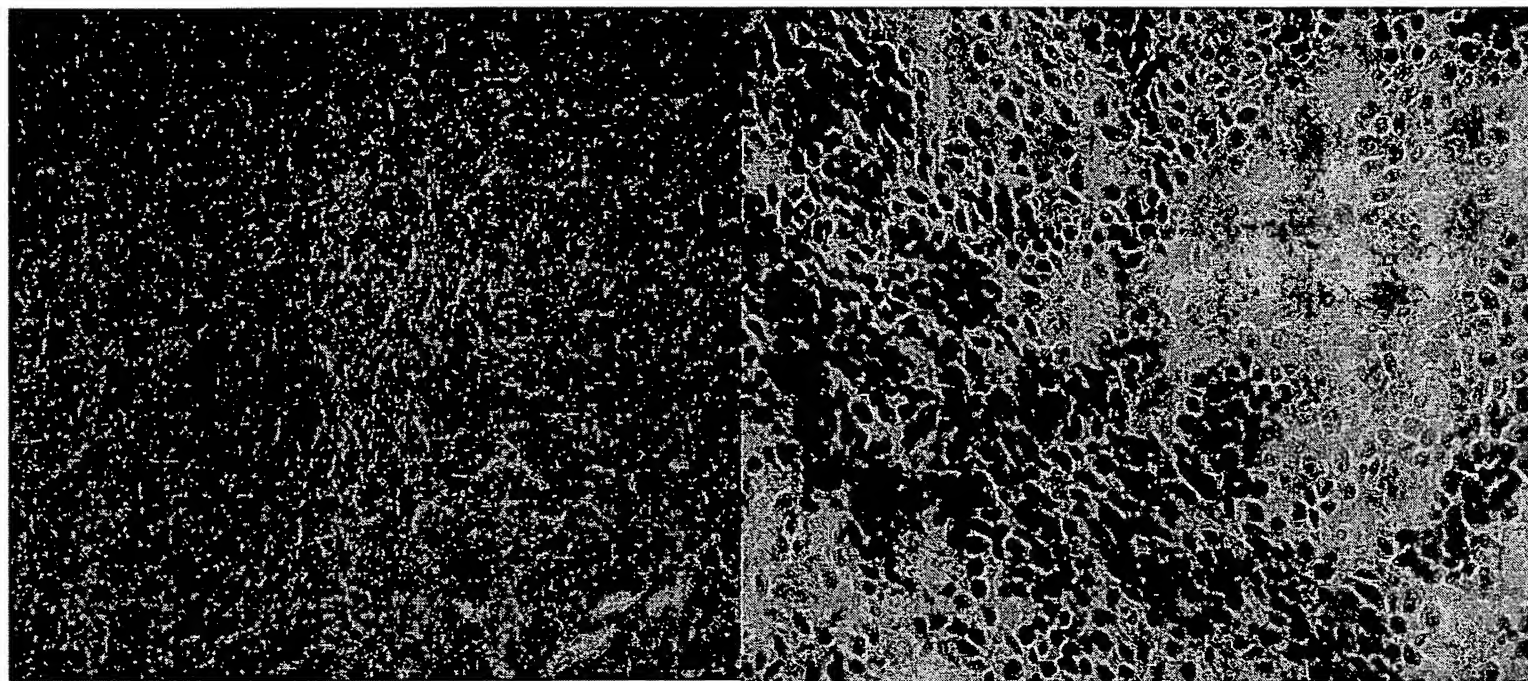


Figure 11



Saline

**ECO-04601
(20 mg/kg)**

Figure 12

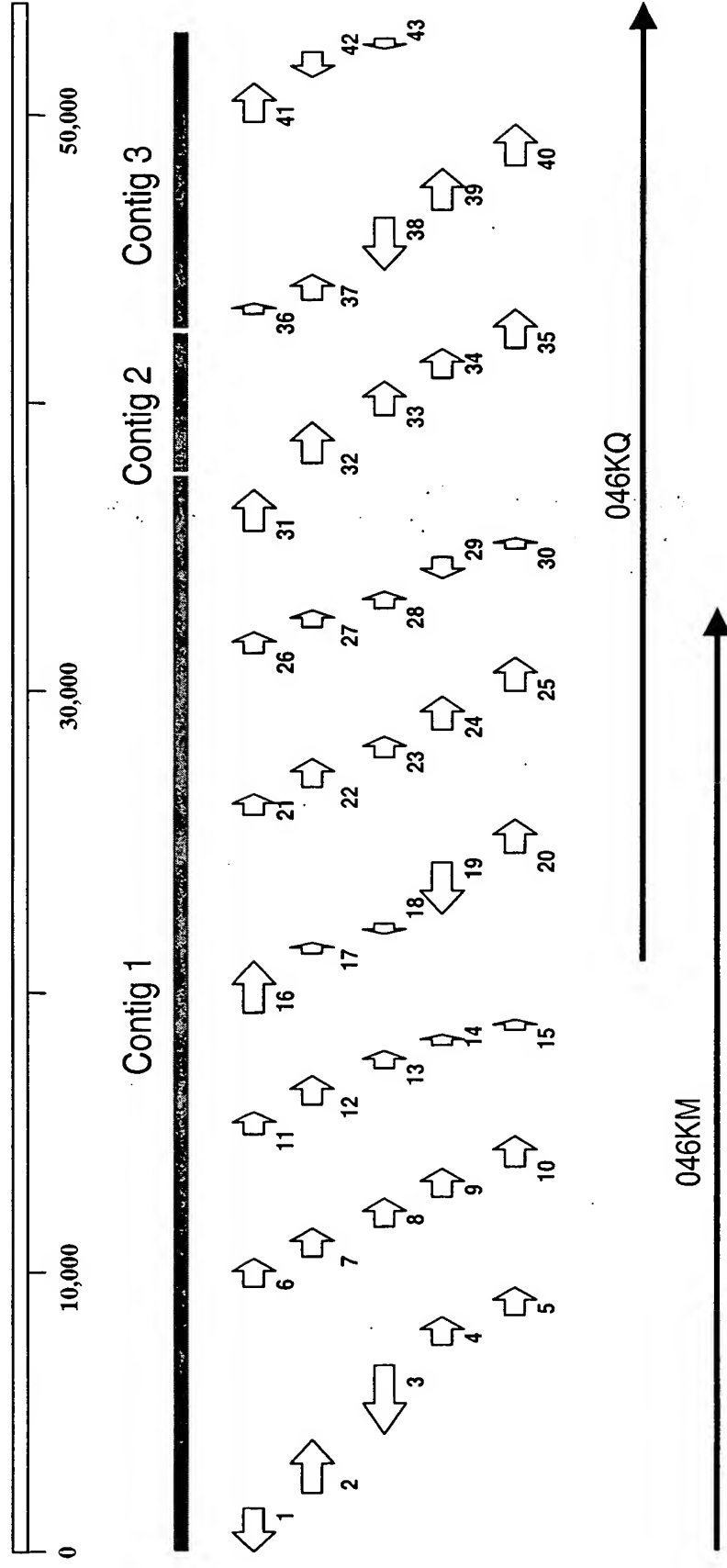


Figure 13

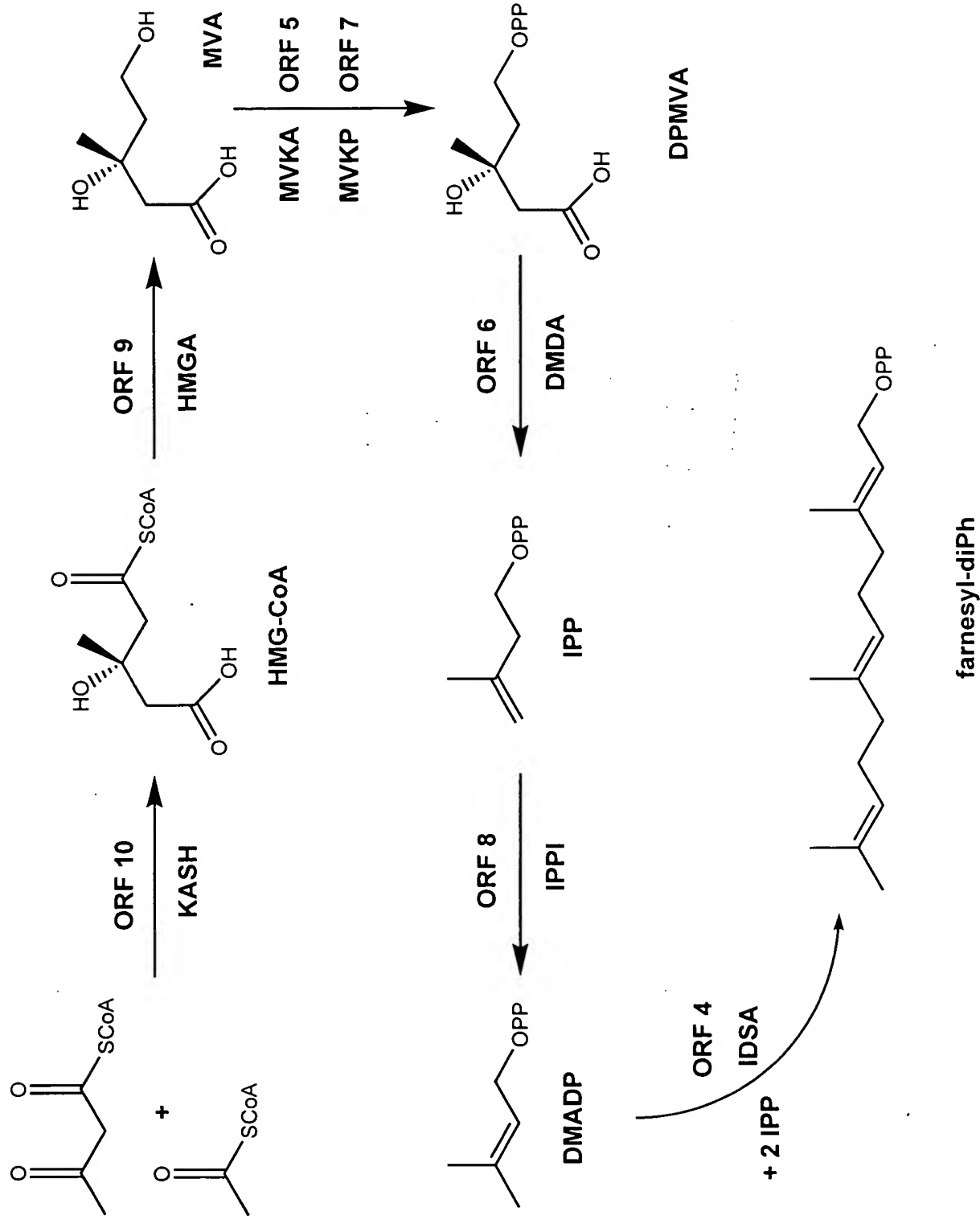


Figure 14

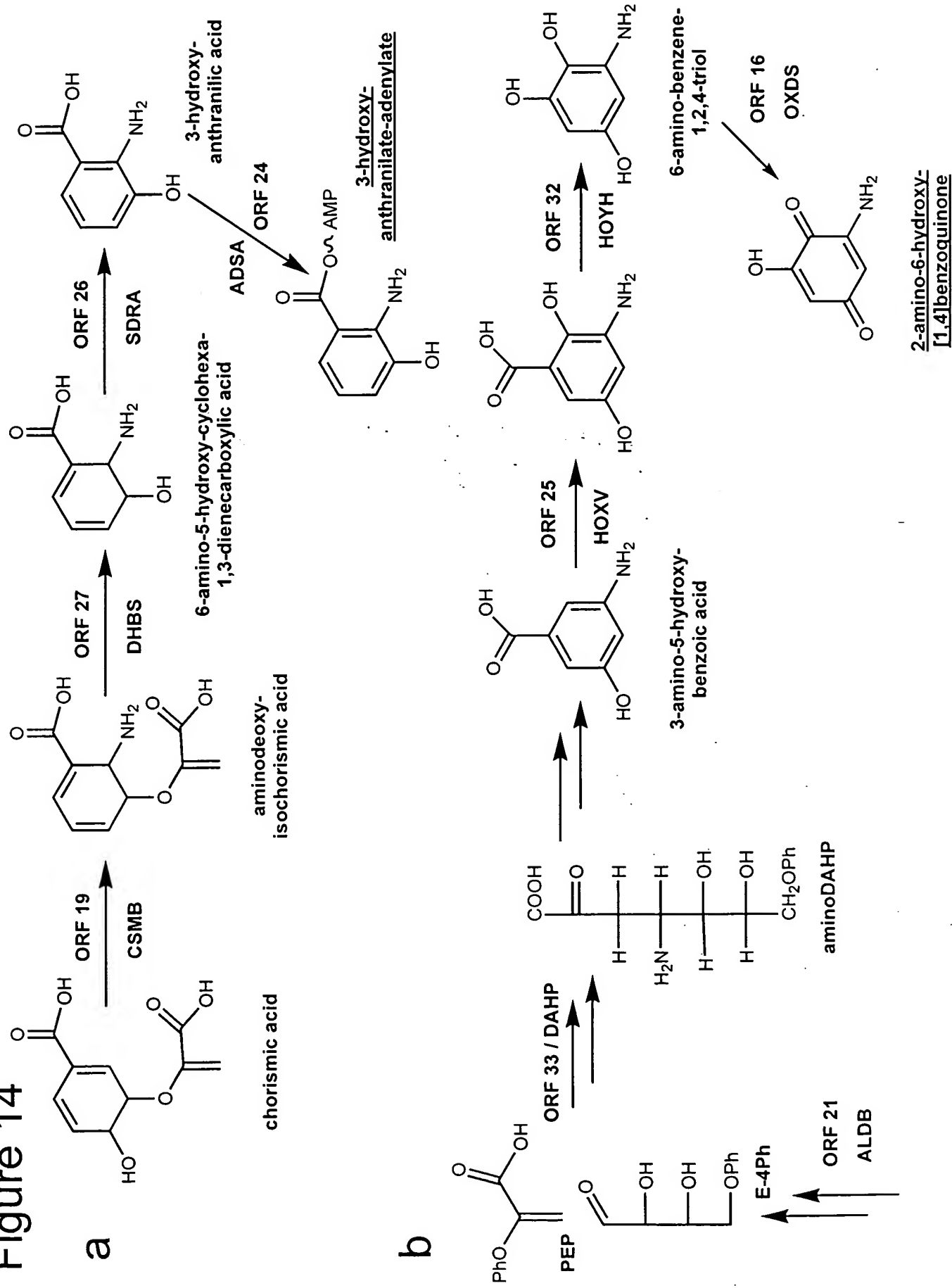
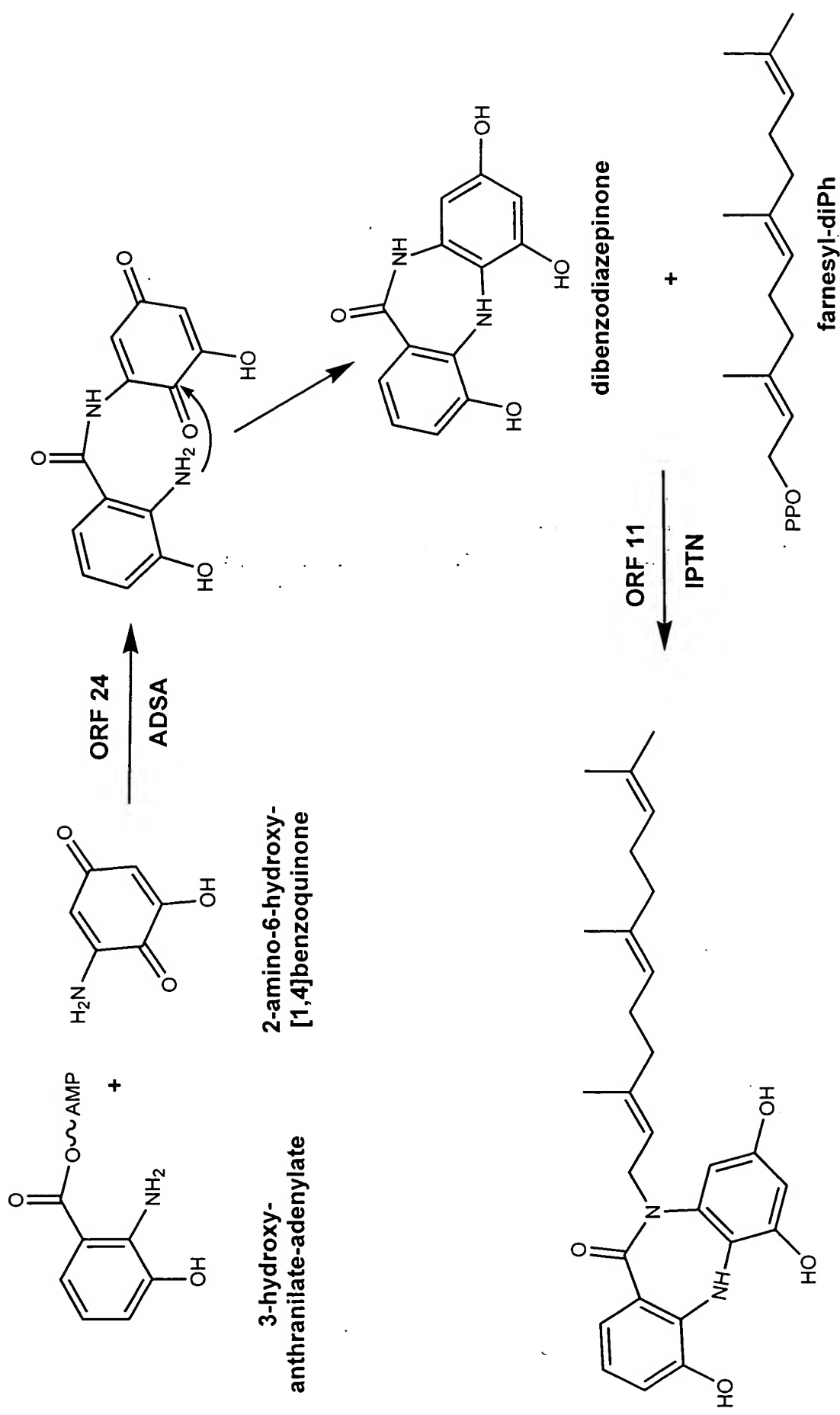


Figure 15



ECO-04601

Figure 16

SEQUENCE LISTING TABLE

SEQ ID NO.	AMINO ACID (AA) or NUCLEIC ACID (NA)	FUNCTION	ORF NO.
1.	NA	CONTIG 1	
2.	AA	ABCC	1
3.	NA	ABCC	
4.	AA	RECH	2
5.	NA	RECH	
6.	AA	REGD	3
7.	NA	REGD	
8.	AA	IDSA	4
9.	NA	IDSA	
10.	AA	MVKA	5
11.	NA	MVKA	
12.	AA	DMDA	6
13.	NA	DMDA	
14.	AA	MVKP	7
15.	NA	MVKP	
16.	AA	IPPI	8
17.	NA	IPPI	
18.	AA	HMGA	9
19.	NA	HMGA	
20.	AA	KASH	10
21.	NA	KASH	
22.	AA	IPTN	11
23.	NA	IPTN	
24.	AA	SPKG	12
25.	NA	SPKG	
26.	AA	RREB	13

27.	NA	RREB	
28.	AA	UNES	14
29.	NA	UNES	
30.	AA	UNEZ	15
31.	NA	UNEZ	
32.	AA	OXDS	16
33.	NA	OXDS	
34.	AA	UNFD	17
35.	NA	UNFD	
36.	AA	UNFA	18
37.	NA	UNFA	
38.	AA	CSMB	19
39.	NA	CSMB	
40.	AA	AAKD	20
41.	NA	AAKD	
42.	AA	ALDB	21
43.	NA	ALDB	
44.	AA	UNFC	22
45.	NA	UNFC	
46.	AA	HYDK	23
47.	NA	HYDK	
48.	AA	ADSA	24
49.	NA	ADSA	
50.	AA	HOXV	25
51.	NA	HOXV	
52.	AA	SDRA	26
53.	NA	SDRA	
54.	AA	DHBS	27
55.	NA	DHBS	
56.	AA	SDRA	28
57.	NA	SDRA	
58.	AA	UNIQ	29
59.	NA	UNIQ	
60.	AA	UNFE	30

61.	NA	UNFE	
62.	AA	EFFT	31
63.	NA	EFFT	
64.	NA	CONTIG 2	
65.	AA	HOYH	32
66.	NA	HOYH	
67.	AA	DAHP	33
68.	NA	DAHP	
69.	AA	REGG	34
70.	NA	REGG	
71.	AA	UNFJ	35
72.	NA	UNFJ	
73.	NA	CONTIG 3	
74.	AA	RECI	36
75.	NA	RECI	
76.	AA	UNIQ	37
77.	NA	UNIQ	
78.	AA	OXAH	38
79.	NA	OXAH	
80.	AA	ABCA	39
81.	NA	ABCA	
82.	AA	UNIQ	40
83.	NA	UNIQ	
84.	AA		41
85.	NA		
86.	AA		42
87.	NA		
88.	AA		43
89.	NA		

Figure 17

RT	Response	Ar/Ht	RFact	ECL	Peak Name	Percent	Comment 1	Comment 2
1.630	4.486E+8	0.026	-----	7.012	Solvent Peak	----	< min rt	
1.874	754	0.024	-----	7.505		----	< min rt	
2.521	1314	0.026	----	8.810		----	< min rt	
8.150	16710	0.041	0.980	14.621	15:0 ISO	26.83	ECL deviates 0.000	Reference 0.000
8.288	3943	0.042	0.977	14.711	15:0 ANTEISO	6.32	ECL deviates 0.000	Reference 0.001
9.767	2378	0.042	0.956	15.627	16: ISO	3.73	ECL deviates 0.001	Reference -0.001
10.086	1692	0.047	0.953	15.819	16:1 CIS 9	2.64	ECL deviates 0.002	Reference
10.385	2413	0.045	0.949	15.999	16:0	3.75	ECL deviates -0.001	Reference -0.003
11.106	11222	0.044	0.941	16.417	16:0 9? METHYL	17.31	ECL deviates 0.001	Reference
11.475	8905	0.046	0.937	16.630	17:0 ISO	13.68	ECL deviates 0.001	Reference 0.000
11.634	11190	0.046	0.936	16.722	17:0 ANTEISO	17.17	ECL deviates 0.000	Reference -0.001
11.757	2741	0.046	0.935	16.793	17:1 CIS 9	4.20	ECL deviates 0.001	Reference
13.468	2898	0.049	0.920	17.771	18:1 CIS 9	4.37	ECL deviates 0.002	Reference

ECL Deviation: 0.001
Total Response: 64093
Percent Named: 100.00%

Reference ECL Shift: 0.001
Total Named: 64093
Total Amount: 61014

Number Reference peaks: 6

Matches:

Library	Sim Index	Entry Name
ACTIN3 1.07	0.293	<i>Micromonospora chalcea</i>

Figure 18

Alignment:		
0.00	%	499
1.00	%	499
1.50	%	499
1.60	%	499
1.60	%	499
1.60	%	499
1.80	%	499
1.80	%	499
2.00	%	499
2.00	%	499

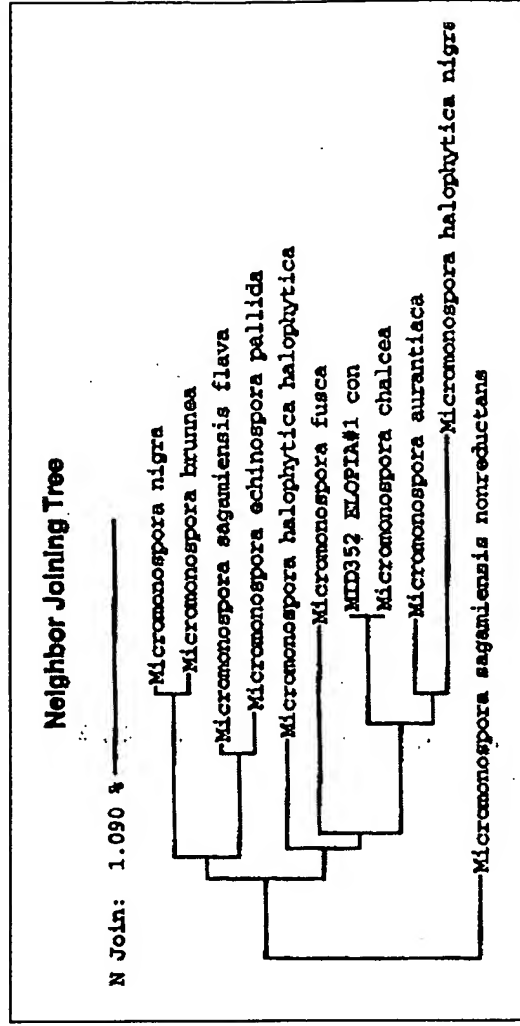


Figure 19

